



SEQUENCE LISTING

<110> Hastings, et al.
<120> Novel Hyaluronan-Binding Proteins and Encoding Genes
<130> PF487
<140> 09/466,778
<141> 1999-12-20
<150> 60/113,871
<151> 1998-12-23
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ggccacgcag acaggccggg tgttcttgca gctgagggtc gccgtggcc atg atg gac 178
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Gln Gly Cys Arg Glu Ile Leu Thr Thr Ala Gly Pro Phe Thr Val Leu
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gtg cca tcc gtc tcc tcc ttc tcc tcc agg acc atg aat gca tcc ctt 274
Val Pro Ser Val Ser Ser Phe Ser Ser Arg Thr Met Asn Ala Ser Leu
      20                25                30                35

gcc cag cag ctc tgt aga cag cac atc atc gca ggg cag cac atc ctg 322
Ala Gln Gln Leu Cys Arg Gln His Ile Ile Ala Gly Gln His Ile Leu
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Glu Asp Thr Arg Thr Gln Gln Thr Arg Arg Trp Trp Thr Leu Ala Gly
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cag gag atc acc gtc acc ttt aac caa ttc acg aaa tac tcc tac aag 418
Gln Glu Ile Thr Val Thr Phe Asn Gln Phe Thr Lys Tyr Ser Tyr Lys
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Tyr Lys Asp Gln Pro Gln Gln Thr Phe Asn Ile Tyr Lys Ala Asn Asn
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Ile Ala Ala Asn Gly Val Phe His Val Val Thr Gly Leu Arg Trp Gln
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gcc ccc tct ggg acc cct ggg gat ccc aag aga act atc gga cag atc 562
Ala Pro Ser Gly Thr Pro Gly Asp Pro Lys Arg Thr Ile Gly Gln Ile
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ctc gcc tct acc gag gcc ttc agc cgc ttt gaa acc atc ctg gag aac 610
Leu Ala Ser Thr Glu Ala Phe Ser Arg Phe Glu Thr Ile Leu Glu Asn
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Cys Gly Leu Pro Ser Ile Leu Asp Gly Pro Gly Pro Phe Thr Val Phe
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cac atc tac aac cac ggc cag ctg acc gtt gag aag ctc atc tcc aag His Ile Tyr Asn 200 200	gln leu thr val glu lys leu ile ser lys 205	802	
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Glu Ser Met Gly Asp Cys Gly Pro Thr Gly Leu Ala Gln His Cys His							
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Leu His Ala Arg Cys Val Ser Gln Glu Gly Val Ala Arg Cys Arg Cys							
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Cys Ser His Pro Asp Arg Gly Gly Cys Ser Glu Asn Ala Glu Cys Val							
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Pro Gly Ser Leu Gly Thr His His Cys Thr Cys His Lys Gly Trp Ser							
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Arg Gly Gly Cys His Thr Asp Ala Leu Cys Ser Tyr Val Gly Pro Gly							
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Glu Val Ala Thr Leu Asn Pro Thr Thr Arg Trp Glu Ile Arg Asn Ile							
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Cys Gly Leu Glu Pro Pro Cys Pro Glu Gly Ser Gln Glu Gln Gly Ser			
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Pro Glu Ala Cys Trp Arg Phe Tyr Pro Lys Phe Trp Thr Ser Pro Pro			
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Thr Thr Trp Lys Pro Ser Cys Cys Pro Gly His Tyr Gly Ser Glu Cys			
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Thr Met Val Thr Cys Thr Cys Leu Pro Asp Tyr Glu Gly Asp Gly Trp			

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Ser Glu His Ala Asn Cys Leu Ser Thr Gly Leu Asn Thr Arg Arg Cys	1735	1740	1745	
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Ser Glu Pro Pro Val Asp Arg Cys Leu Gly Gln Pro Pro Cys His	1765	1770	1775	
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Val Phe His Leu Gln Ala Thr Ser Gly Pro Tyr Gly Leu Asn Phe Ser	1800	1805	1810	
gag gct gag gcg gca tgc gaa gca cag gga gcc gtc ctt gct tca ttc				5650
Glu Ala Glu Ala Ala Cys Glu Ala Gln Gly Ala Val Leu Ala Ser Phe	1815	1820	1825	
cct cag ctc tct gct gcc cag cag ctg ggc ttc cac ctg tgc ctc atg				5698
Pro Gln Leu Ser Ala Ala Gln Gln Leu Gly Phe His Leu Cys Leu Met	1830	1835	1840	
ggc tgg ctg gcc aat ggc tcc act gcc cac cct gtg gtt ttc cct gtg				5746
Gly Trp Leu Ala Asn Gly Ser Thr Ala His Pro Val Val Phe Pro Val	1845	1850	1855	
gcg gac tgt ggc aat ggt cgg gtg ggc ata gtc agc ctg ggt gcc cgc				5794
Ala Asp Cys Gly Asn Gly Arg Val Gly Ile Val Ser Leu Gly Ala Arg	1860	1865	1870	1875
aag aac ctc tca gaa cgc tgg gat gcc tac tgc ttc cgt gtg caa gat				5842
Lys Asn Leu Ser Glu Arg Trp Asp Ala Tyr Cys Phe Arg Val Gln Asp	1880	1885	1890	
gtg gcc tgc cga tgc cga aat ggc ttc gtg ggt gac ggg atc agc acg				5890
Val Ala Cys Arg Cys Arg Asn Gly Phe Val Gly Asp Gly Ile Ser Thr	1895	1900	1905	
tgc aat ggg aag ctg ctg gat gtg ctg gct gcc act gcc aac ttc tcc				5938
Cys Asn Gly Lys Leu Leu Asp Val Leu Ala Ala Thr Ala Asn Phe Ser	1910	1915	1920	
acc ttc tat ggg atg cta ttg ggc tat gcc aat gcc acc cag cgg ggt				5986
Thr Phe Tyr Gly Met Leu Leu Gly Tyr Ala Asn Ala Thr Gln Arg Gly	1925	1930	1935	
ctc gac ttc ctg gac ttc ctg gat gat gag ctc acg tat aag aca ctc				6034
Leu Asp Phe Leu Asp Phe Leu Asp Asp Glu Leu Thr Tyr Lys Thr Leu	1940	1945	1950	1955
ttc gtc cct gtc aat gaa ggc ttt gtg gac aac atg acg ctg agt ggc				6082
Phe Val Pro Val Asn Glu Gly Phe Val Asp Asn Met Thr Leu Ser Gly				

1960	1965	1970	
cca aac ttg gag ctg cat gcc tcc aac gcc acc ctc cta agt gcc aac Pro Asn Leu Glu Leu His Ala Ser Asn Ala Thr Leu Leu Ser Ala Asn 1975 1980 1985			6130
gcc agc cag ggg aag ttg ctt ccg gcc cac tca ggc ctc agc ctc atc Ala Ser Gln Gly Lys Leu Leu Pro Ala His Ser Gly Leu Ser Leu Ile 1990 1995 2000			6178
atc agt gac gca ggc cct gac aac agt tcc tgg gcc cct gtg gcc cca Ile Ser Asp Ala Gly Pro Asp Asn Ser Ser Trp Ala Pro Val Ala Pro 2005 2010 2015			6226
ggg aca gtt gtg gtt agc cgt atc att gtg tgg gac atc atg gcc ttc Gly Thr Val Val Val Ser Arg Ile Ile Val Trp Asp Ile Met Ala Phe 2020 2025 2030 2035			6274
aat ggc atc atc cat gct ctg gcc agc ccc ctc ctg gca ccc cca cag Asn Gly Ile Ile His Ala Leu Ala Ser Pro Leu Leu Ala Pro Pro Gln 2040 2045 2050			6322
ccc cag gca gtg ctg gcg cnt gaa gcc cca cct gtg gcg gca ggc gtg Pro Gln Ala Val Leu Ala Xaa Glu Ala Pro Pro Val Ala Ala Gly Val 2055 2060 2065			6370
ggg gct gtg ctt gcc gct gga gca ctg ctt ggc ttg gtg gcc gga gct Gly Ala Val Leu Ala Ala Gly Ala Leu Leu Gly Leu Val Ala Gly Ala 2070 2075 2080			6418
ctc tac ctc cgt gcc cga ggc aag ccc atg ggc ttt ggc ttc tct gcc Leu Tyr Leu Arg Ala Arg Gly Lys Pro Met Gly Phe Gly Phe Ser Ala 2085 2090 2095			6466
ttc cag gcg gaa gat gat gct gat gac gan ttc tca ccg tgg caa gaa Phe Gln Ala Glu Asp Asp Ala Asp Asp Xaa Phe Ser Pro Trp Gln Glu 2100 2105 2110 2115			6514
ggg acc aac ccc acn ttg gtn tnt gtc ccc aac cct gtc ttt ggc agc Gly Thr Asn Pro Xaa Leu Xaa Xaa Val Pro Asn Pro Val Phe Gly Ser 2120 2125 2130			6562
gac acc ttt tgt gaa ccc ttc gat gac tca ctg ctg gag gag gac ttc Asp Thr Phe Cys Glu Pro Phe Asp Asp Ser Leu Leu Glu Glu Asp Phe 2135 2140 2145			6610
cct gac acc cag agg atc ctc aca gtc aag tga cgaggctggg gctgaaagca Pro Asp Thr Gln Arg Ile Leu Thr Val Lys 2150 2155			6663
gaagcatgca cagggaggag accanttttta ttgcttgtct ggggtggatgg ggcaggaggg			6723
nctgaggggcc tgtcccagac aatannngtn ccctcgag			6761

<210> 2
 <211> 2157
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (2058)
 <223> Xaa equals any of the naturally occurring L-amino acids

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<220>
<221> MISC_FEATURE
<222> (2109)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> MISC_FEATURE
<222> (2120)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> MISC_FEATURE
<222> (2122)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> MISC_FEATURE
<222> (2123)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 2
Met Met Asp Gln Gly Cys Arg Glu Ile Leu Thr Thr Ala Gly Pro Phe
 1          5          10          15
Thr Val Leu Val Pro Ser Val Ser Ser Phe Ser Ser Arg Thr Met Asn
          20          25          30
Ala Ser Leu Ala Gln Gln Leu Cys Arg Gln His Ile Ile Ala Gly Gln
          35          40          45
His Ile Leu Glu Asp Thr Arg Thr Gln Gln Thr Arg Arg Trp Trp Thr
          50          55          60
Leu Ala Gly Gln Glu Ile Thr Val Thr Phe Asn Gln Phe Thr Lys Tyr
65          70          75          80
Ser Tyr Lys Tyr Lys Asp Gln Pro Gln Gln Thr Phe Asn Ile Tyr Lys
          85          90          95
Ala Asn Asn Ile Ala Ala Asn Gly Val Phe His Val Val Thr Gly Leu
          100          105          110
Arg Trp Gln Ala Pro Ser Gly Thr Pro Gly Asp Pro Lys Arg Thr Ile
          115          120          125
Gly Gln Ile Leu Ala Ser Thr Glu Ala Phe Ser Arg Phe Glu Thr Ile
          130          135          140
Leu Glu Asn Cys Gly Leu Pro Ser Ile Leu Asp Gly Pro Gly Pro Phe
145          150          155          160
Thr Val Phe Ala Pro Ser Asn Glu Ala Val Asp Ser Leu Arg Asp Gly
          165          170          175
Arg Leu Ile Tyr Leu Phe Thr Ala Gly Leu Ser Lys Leu Gln Glu Leu
          180          185          190
Val Arg Tyr His Ile Tyr Asn His Gly Gln Leu Thr Val Glu Lys Leu
          195          200          205
Ile Ser Lys Gly Arg Ile Leu Thr Met Ala Asn Gln Val Leu Ala Val
210          215          220

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Asn Ile Ser Glu Glu Gly Arg Ile Leu Leu Gly Pro Glu Gly Val Pro
 225 230 235 240
 Leu Gln Arg Val Asp Val Met Ala Ala Asn Gly Val Ile His Met Leu
 245 250 255
 Asp Gly Ile Leu Leu Pro Pro Thr Ile Leu Pro Ile Leu Pro Lys His
 260 265 270
 Cys Ser Glu Glu Gln His Lys Ile Val Ala Gly Ser Cys Val Asp Cys
 275 280 285
 Gln Ala Leu Asn Thr Ser Thr Cys Pro Pro Asn Ser Val Lys Leu Asp
 290 295 300
 Ile Phe Pro Lys Glu Cys Val Tyr Ile His Asp Pro Thr Gly Leu Asn
 305 310 315 320
 Val Leu Lys Lys Gly Cys Ala Ser Tyr Cys Asn Gln Thr Ile Met Glu
 325 330 335
 Gln Gly Cys Cys Lys Gly Phe Phe Gly Pro Asp Cys Thr Gln Cys Pro
 340 345 350
 Gly Gly Phe Ser Asn Pro Cys Tyr Gly Lys Gly Asn Cys Ser Asp Gly
 355 360 365
 Ile Gln Gly Asn Gly Ala Cys Leu Cys Phe Pro Asp Tyr Lys Gly Ile
 370 375 380
 Ala Cys His Ile Cys Ser Asn Pro Asn Lys His Gly Glu Gln Cys Gln
 385 390 395 400
 Glu Asp Cys Gly Cys Val His Gly Leu Cys Asp Asn Arg Pro Gly Ser
 405 410 415
 Gly Gly Val Cys Gln Gln Gly Thr Cys Ala Pro Gly Phe Ser Gly Arg
 420 425 430
 Phe Cys Asn Glu Ser Met Gly Asp Cys Gly Pro Thr Gly Leu Ala Gln
 435 440 445
 His Cys His Leu His Ala Arg Cys Val Ser Gln Glu Gly Val Ala Arg
 450 455 460
 Cys Arg Cys Leu Asp Gly Phe Glu Gly Asp Gly Phe Ser Cys Thr Pro
 465 470 475 480
 Ser Asn Pro Cys Ser His Pro Asp Arg Gly Gly Cys Ser Glu Asn Ala
 485 490 495
 Glu Cys Val Pro Gly Ser Leu Gly Thr His His Cys Thr Cys His Lys
 500 505 510
 Gly Trp Ser Gly Asp Gly Arg Val Cys Val Ala Ile Asp Glu Cys Glu
 515 520 525
 Leu Asp Val Arg Gly Gly Cys His Thr Asp Ala Leu Cys Ser Tyr Val
 530 535 540
 Gly Pro Gly Gln Ser Arg Cys Thr Cys Lys Leu Gly Phe Ala Gly Asp
 545 550 555 560
 Gly Tyr Gln Cys Ser Pro Ile Asp Pro Cys Arg Ala Gly Asn Gly Gly

Gly Thr Leu Cys Glu Pro Cys Pro Gly Gly Leu Gly Gly Val Cys Ser
 915 920 925
 Gly His Gly Gln Cys Gln Asp Arg Phe Leu Gly Ser Gly Glu Cys His
 930 935 940
 Cys His Glu Gly Phe His Gly Thr Ala Cys Glu Val Cys Glu Leu Gly
 945 950 955 960
 Arg Tyr Gly Pro Asn Cys Thr Gly Val Cys Asp Cys Ala His Gly Leu
 965 970 975
 Cys Gln Glu Gly Leu Gln Gly Asp Gly Ser Cys Val Cys Asn Val Gly
 980 985 990
 Trp Gln Gly Leu Arg Cys Asp Gln Lys Ile Thr Ser Pro Gln Cys Pro
 995 1000 1005
 Arg Lys Cys Asp Pro Asn Ala Asn Cys Val Gln Asp Ser Ala Gly Ala
 1010 1015 1020
 Ser Thr Cys Ala Cys Ala Ala Gly Tyr Ser Gly Asn Gly Ile Phe Cys
 1025 1030 1035 1040
 Ser Glu Val Asp Pro Cys Ala His Gly His Gly Gly Cys Ser Pro His
 1045 1050 1055
 Ala Asn Cys Thr Lys Val Ala Pro Gly Gln Arg Thr Cys Thr Cys Gln
 1060 1065 1070
 Asp Gly Tyr Met Gly Asp Gly Glu Leu Cys Gln Glu Ile Asn Ser Cys
 1075 1080 1085
 Leu Ile His His Gly Gly Cys His Ile His Ala Glu Cys Ile Pro Thr
 1090 1095 1100
 Gly Pro Gln Gln Val Ser Cys Ser Cys Arg Glu Gly Tyr Ser Gly Asp
 1105 1110 1115 1120
 Gly Ile Arg Thr Cys Glu Leu Leu Asp Pro Cys Ser Lys Asn Asn Gly
 1125 1130 1135
 Gly Cys Ser Pro Tyr Ala Thr Cys Lys Ser Thr Gly Asp Gly Gln Arg
 1140 1145 1150
 Thr Cys Thr Cys Asp Thr Ala His Thr Val Gly Asp Gly Leu Thr Cys
 1155 1160 1165
 Arg Ala Arg Val Gly Leu Glu Leu Leu Arg Asp Lys His Ala Ser Phe
 1170 1175 1180
 Phe Ser Leu Arg Leu Leu Glu Tyr Lys Glu Leu Lys Gly Asp Gly Pro
 1185 1190 1195 1200
 Phe Thr Ile Phe Val Pro His Ala Asp Leu Met Ser Asn Leu Ser Gln
 1205 1210 1215
 Asp Glu Leu Ala Arg Ile Arg Ala His Arg Gln Leu Val Phe Arg Tyr
 1220 1225 1230
 His Val Val Gly Cys Arg Arg Leu Arg Ser Glu Asp Leu Leu Glu Gln
 1235 1240 1245

Gly Tyr Ala Thr Ala Leu Ser Gly His Pro Leu Arg Phe Ser Glu Arg
 1250 1255 1260
 Glu Gly Ser Ile Tyr Leu Asn Asp Phe Ala Arg Val Val Ser Ser Asp
 1265 1270 1275 1280
 His Glu Ala Val Asn Gly Ile Leu His Phe Ile Asp Arg Val Leu Leu
 1285 1290 1295
 Pro Pro Glu Ala Leu His Trp Glu Pro Asp Asp Ala Pro Ile Pro Arg
 1300 1305 1310
 Arg Asn Val Thr Ala Ala Ala Gln Gly Phe Gly Tyr Lys Ile Phe Ser
 1315 1320 1325
 Gly Leu Leu Lys Val Ala Gly Leu Leu Pro Leu Leu Arg Glu Ala Ser
 1330 1335 1340
 His Arg Pro Phe Thr Met Leu Trp Pro Thr Asp Ala Ala Phe Arg Ala
 1345 1350 1355 1360
 Leu Pro Pro Asp Arg Gln Ala Trp Leu Tyr His Glu Asp His Arg Asp
 1365 1370 1375
 Lys Leu Ala Ala Ile Leu Arg Gly His Met Ile Arg Asn Val Glu Ala
 1380 1385 1390
 Leu Ala Ser Asp Leu Pro Asn Leu Gly Pro Leu Arg Thr Met His Gly
 1395 1400 1405
 Thr Pro Ile Ser Phe Ser Cys Ser Arg Thr Arg Pro Gly Glu Leu Met
 1410 1415 1420
 Val Gly Glu Asp Asp Ala Arg Ile Val Gln Arg His Leu Pro Phe Glu
 1425 1430 1435 1440
 Gly Gly Leu Ala Tyr Gly Ile Asp Gln Leu Leu Glu Pro Pro Gly Leu
 1445 1450 1455
 Gly Ala Arg Cys Asp His Phe Glu Thr Arg Pro Leu Arg Leu Asn Thr
 1460 1465 1470
 Cys Ser Ile Cys Gly Leu Glu Pro Pro Cys Pro Glu Gly Ser Gln Glu
 1475 1480 1485
 Gln Gly Ser Pro Glu Ala Cys Trp Arg Phe Tyr Pro Lys Phe Trp Thr
 1490 1495 1500
 Ser Pro Pro Leu His Ser Leu Gly Leu Arg Ser Val Trp Val His Pro
 1505 1510 1515 1520
 Ser Leu Trp Gly Arg Pro Gln Gly Leu Gly Arg Gly Cys His Arg Asn
 1525 1530 1535
 Cys Val Thr Thr Thr Trp Lys Pro Ser Cys Cys Pro Gly His Tyr Gly
 1540 1545 1550
 Ser Glu Cys Gln Ala Cys Pro Gly Gly Pro Ser Ser Pro Cys Ser Asp
 1555 1560 1565
 Arg Gly Val Cys Met Asp Gly Met Ser Gly Ser Gly Gln Cys Leu Cys
 1570 1575 1580
 Arg Ser Gly Phe Ala Gly Thr Ala Cys Glu Leu Cys Ala Pro Gly Ala

1585	1590	1595	1600
Phe Gly Pro His Cys 1605	Gln Ala Cys Arg Cys 1610	Thr Val His Gly Arg 1615	Cys
Asp Glu Gly Leu Gly Gly Ser Gly Ser Cys Phe Cys Asp Glu Gly Trp 1620 1625 1630			
Thr Gly Pro Arg Cys Glu Val Gln Leu Glu Leu Gln Pro Val Cys Thr 1635 1640 1645			
Pro Pro Cys Ala Pro Glu Ala Val Cys Arg Ala Gly Asn Ser Cys Glu 1650 1655 1660			
Cys Ser Leu Gly Tyr Glu Gly Asp Gly Arg Val Cys Thr Val Ala Asp 1665 1670 1675 1680			
Leu Cys Gln Asp Gly His Gly Gly Cys Ser Glu His Ala Asn Cys Ser 1685 1690 1695			
Gln Val Gly Thr Met Val Thr Cys Thr Cys Leu Pro Asp Tyr Glu Gly 1700 1705 1710			
Asp Gly Trp Ser Cys Arg Ala Arg Asn Pro Cys Thr Asp Gly His Arg 1715 1720 1725			
Gly Gly Cys Ser Glu His Ala Asn Cys Leu Ser Thr Gly Leu Asn Thr 1730 1735 1740			
Arg Arg Cys Glu Cys His Ala Gly Tyr Val Gly Asp Gly Leu Gln Cys 1745 1750 1755 1760			
Leu Glu Glu Ser Glu Pro Pro Val Asp Arg Cys Leu Gly Gln Pro Pro 1765 1770 1775			
Pro Cys His Ser Asp Ala Met Cys Thr Asp Leu His Phe Gln Glu Lys 1780 1785 1790			
Arg Ala Gly Val Phe His Leu Gln Ala Thr Ser Gly Pro Tyr Gly Leu 1795 1800 1805			
Asn Phe Ser Glu Ala Glu Ala Ala Cys Glu Ala Gln Gly Ala Val Leu 1810 1815 1820			
Ala Ser Phe Pro Gln Leu Ser Ala Ala Gln Gln Leu Gly Phe His Leu 1825 1830 1835 1840			
Cys Leu Met Gly Trp Leu Ala Asn Gly Ser Thr Ala His Pro Val Val 1845 1850 1855			
Phe Pro Val Ala Asp Cys Gly Asn Gly Arg Val Gly Ile Val Ser Leu 1860 1865 1870			
Gly Ala Arg Lys Asn Leu Ser Glu Arg Trp Asp Ala Tyr Cys Phe Arg 1875 1880 1885			
Val Gln Asp Val Ala Cys Arg Cys Arg Asn Gly Phe Val Gly Asp Gly 1890 1895 1900			
Ile Ser Thr Cys Asn Gly Lys Leu Leu Asp Val Leu Ala Ala Thr Ala 1905 1910 1915 1920			
Asn Phe Ser Thr Phe Tyr Gly Met Leu Leu Gly Tyr Ala Asn Ala Thr 1925 1930 1935			

Gln Arg Gly Leu Asp Phe Leu Asp Phe Leu Asp Asp Glu Leu Thr Tyr
 1940 1945 1950
 Lys Thr Leu Phe Val Pro Val Asn Glu Gly Phe Val Asp Asn Met Thr
 1955 1960 1965
 Leu Ser Gly Pro Asn Leu Glu Leu His Ala Ser Asn Ala Thr Leu Leu
 1970 1975 1980
 Ser Ala Asn Ala Ser Gln Gly Lys Leu Leu Pro Ala His Ser Gly Leu
 1985 1990 1995 2000
 Ser Leu Ile Ile Ser Asp Ala Gly Pro Asp Asn Ser Ser Trp Ala Pro
 2005 2010 2015
 Val Ala Pro Gly Thr Val Val Val Ser Arg Ile Ile Val Trp Asp Ile
 2020 2025 2030
 Met Ala Phe Asn Gly Ile Ile His Ala Leu Ala Ser Pro Leu Leu Ala
 2035 2040 2045
 Pro Pro Gln Pro Gln Ala Val Leu Ala Xaa Glu Ala Pro Pro Val Ala
 2050 2055 2060
 Ala Gly Val Gly Ala Val Leu Ala Ala Gly Ala Leu Leu Gly Leu Val
 2065 2070 2075 2080
 Ala Gly Ala Leu Tyr Leu Arg Ala Arg Gly Lys Pro Met Gly Phe Gly
 2085 2090 2095
 Phe Ser Ala Phe Gln Ala Glu Asp Asp Ala Asp Asp Xaa Phe Ser Pro
 2100 2105 2110
 Trp Gln Glu Gly Thr Asn Pro Xaa Leu Xaa Xaa Val Pro Asn Pro Val
 2115 2120 2125
 Phe Gly Ser Asp Thr Phe Cys Glu Pro Phe Asp Asp Ser Leu Leu Glu
 2130 2135 2140
 Glu Asp Phe Pro Asp Thr Gln Arg Ile Leu Thr Val Lys
 2145 2150 2155

 <210> 3
 <211> 193
 <212> PRT
 <213> Homo sapiens

 <400> 3
 Met Tyr Trp Asp Thr Gly Trp Gly Lys Asp Gly His Asn Ser Trp Arg
 1 5 10 15
 Ala Ala Gly Val Tyr His Arg Ala Arg Ser Gly Lys Tyr Lys Thr Tyr
 20 25 30
 Ala Ala Lys Ala Val Cys Gly Gly His Ala Thr Tyr Lys Ala Ala Arg
 35 40 45
 Lys Gly His Val Cys Ala Ala Gly Trp Met Ala Lys Gly Arg Val Gly
 50 55 60
 Tyr Val Lys Gly Asn Cys Gly Gly Lys Thr Gly Asp Tyr Gly Arg Asn
 65 70 75 80


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<220>
<221> misc_feature
<222> (1485)
<223> n equals a, t, g or c

<220>
<221> misc_feature
<222> (1509)
<223> n equals a, t, g or c

<220>
<221> misc_feature
<222> (1511)
<223> n equals a, t, g or c

<220>
<221> misc_feature
<222> (1514)
<223> n equals a, t, g or c

<400> 4
gagcagccca actgtagcca ggttaggaaca atg gtc act tgt acc tgc ctg ccc 54
                               Met Val Thr Cys Thr Cys Leu Pro
                               1                               5

gac tac gag ggt gat ggc tgg agc tgc cgg gcc cgc aac ccc tgc aca 102
Asp Tyr Glu Gly Asp Gly Trp Ser Cys Arg Ala Arg Asn Pro Cys Thr
10                               15                               20

gat ggc cac cgc ggg ggc tgc agc gag cac gcc aac tgc ttg agc acc 150
Asp Gly His Arg Gly Gly Cys Ser Glu His Ala Asn Cys Leu Ser Thr
25                               30                               35                               40

ggc ctg aac aca cgg cgc tgt gag tgc cac gca ggc tac gta ggc gat 198
Gly Leu Asn Thr Arg Arg Cys Glu Cys His Ala Gly Tyr Val Gly Asp
45                               50                               55

gga ctg cag tgt ctg gag gag tcg gaa cca cct gtg gac cgc tgc ttg 246
Gly Leu Gln Cys Leu Glu Glu Ser Glu Pro Pro Val Asp Arg Cys Leu
60                               65                               70

ggc cag cca ccg ccc tgc cac tca gat gcc atg tgc act gac ctg cac 294
Gly Gln Pro Pro Cys His Ser Asp Ala Met Cys Thr Asp Leu His
75                               80                               85

ttc cag gag aaa cgg gct ggc gtt ttc cac ctc cag gcc acc agc ggc 342
Phe Gln Glu Lys Arg Ala Gly Val Phe His Leu Gln Ala Thr Ser Gly
90                               95                               100

cct tat ggt ctg aac ttt tcg gag gct gag gcg gca tgc gaa gca cag 390
Pro Tyr Gly Leu Asn Phe Ser Glu Ala Glu Ala Ala Cys Glu Ala Gln
105                               110                               115                               120

gga gcc gtc ctt gct tca ttc cct cag ctc tct gct gcc cag cag ctg 438
Gly Ala Val Leu Ala Ser Phe Pro Gln Leu Ser Ala Ala Gln Gln Leu
125                               130                               135

ggc ttc cac ctg tgc ctc atg ggc tgg ctg gcc aat ggc tcc act gcc 486
Gly Phe His Leu Cys Leu Met Gly Trp Leu Ala Asn Gly Ser Thr Ala
140                               145                               150

cac cct gtg gtt ttc cct gtg gcg gac tgt ggc aat ggt cgg gtg ggc 534
His Pro Val Val Phe Pro Val Ala Asp Cys Gly Asn Gly Arg Val Gly
155                               160                               165

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ata gtc agc ctg ggt gcc cgc aag aac ctc tca gaa cgc tgg gat gcc Ile Val Ser Leu Gly Ala Arg Lys Asn Leu Ser Glu Arg Trp Asp Ala 170 175 180	582
tac tgc ttc cgt gtg caa gat gtg gcc tgc cga tgc cga aat ggc ttc Tyr Cys Phe Arg Val Gln Asp Val Ala Cys Arg Cys Arg Asn Gly Phe 185 190 195 200	630
gtg ggt gac ggg atc agc acg tgc aat ggg aag ctg ctg gat gtg ctg Val Gly Asp Gly Ile Ser Thr Cys Asn Gly Lys Leu Leu Asp Val Leu 205 210 215	678
gct gcc act gcc aac ttc tcc acc ttc tat ggg atg cta ttg ggc tat Ala Ala Thr Asn Phe Ser Thr Phe Tyr Gly Met Leu Leu Gly Tyr 220 225 230	726
gcc aat gcc acc cag cgg ggt ctc gac ttc ctg gac ttc ctg gat gat Ala Asn Ala Thr Gln Arg Gly Leu Asp Phe Leu Asp Phe Leu Asp Asp 235 240 245	774
gag ctc acg tat aag aca ctc ttc gtc cct gtc aat gaa ggc ttt gtg Glu Leu Thr Tyr Lys Thr Leu Phe Val Pro Val Asn Glu Gly Phe Val 250 255 260	822
gac aac atg acg ctg agt ggc cca aac ttg gag ctg cat gcc tcc aac Asp Asn Met Thr Leu Ser Gly Pro Asn Leu Glu Leu His Ala Ser Asn 265 270 275 280	870
gcc acc ctc cta agt gcc aac gcc agc cag ggg aag ttg ctt ccg gcc Ala Thr Leu Leu Ser Ala Asn Ala Ser Gln Gly Lys Leu Leu Pro Ala 285 290 295	918
cac tca ggc ctc agc ctc atc atc agt gac gca ggc cct gac aac agt His Ser Gly Leu Ser Leu Ile Ile Ser Asp Ala Gly Pro Asp Asn Ser 300 305 310	966
tcc tgg gcc cct gtg gcc cca ggg aca gtt gtg gtt agc cgt atc att Ser Trp Ala Pro Val Ala Pro Gly Thr Val Val Val Ser Arg Ile Ile 315 320 325	1014
gtg tgg gac atc atg gcc ttc aat ggc atc atc cat gct ctg gcc agc Val Trp Asp Ile Met Ala Phe Asn Gly Ile Ile His Ala Leu Ala Ser 330 335 340	1062
ccc ctc ctg gca ccc cca cag ccc cag gca gtg ctg gcg cnt gaa gcc Pro Leu Leu Ala Pro Pro Gln Pro Gln Ala Val Leu Ala Xaa Glu Ala 345 350 355 360	1110
cca cct gtg gcg gca ggc gtg ggg gct gtg ctt gcc gct gga gca ctg Pro Pro Val Ala Ala Gly Val Gly Ala Val Leu Ala Ala Gly Ala Leu 365 370 375	1158
ctt ggc ttg gtg gcc gga gct ctc tac ctc cgt gcc cga ggc aag ccc Leu Gly Leu Val Ala Gly Ala Leu Tyr Leu Arg Ala Arg Gly Lys Pro 380 385 390	1206
atg ggc ttt ggc ttc tct gcc ttc cag gcg gaa gat gat gct gat gac Met Gly Phe Gly Phe Ser Ala Phe Gln Ala Glu Asp Asp Ala Asp Asp 395 400 405	1254
gan ttc tca ccg tgg caa gaa ggg acc aac ccc acn ttg gtn tnt gtc Xaa Phe Ser Pro Trp Gln Glu Gly Thr Asn Pro Xaa Leu Xaa Xaa Val 410 415 420	1302

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ccc aac cct gtc ttt ggc agc gac acc ttt tgt gaa ccc ttc gat gac 1350
Pro Asn Pro Val Phe Gly Ser Asp Thr Phe Cys Glu Pro Phe Asp Asp
425 430 435 440

tca ctg ctg gag gag gac ttc cct gac acc cag agg atc ctc aca gtc 1398
Ser Leu Leu Glu Glu Asp Phe Pro Asp Thr Gln Arg Ile Leu Thr Val
445 450 455

aag tga cgaggctggg gctgaaagca gaagcatgca cagggaggag accantttta 1454
Lys

ttgcttgtct ggggtggatgg ggcaggaggg nctgagggcc tgtcccagac aatannngtn 1514

ccctcgag 1522

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<210> 5
<211> 457
<212> PRT
<213> Homo sapiens

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<220>
<221> MISC_FEATURE
<222> (358)
<223> Xaa equals any of the naturally occurring L-amino acids

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<220>
<221> MISC_FEATURE
<222> (409)
<223> Xaa equals any of the naturally occurring L-amino acids

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<220>
<221> MISC_FEATURE
<222> (420)
<223> Xaa equals any of the naturally occurring L-amino acids

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<220>
<221> MISC_FEATURE
<222> (422)
<223> Xaa equals any of the naturally occurring L-amino acids

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<220>
<221> MISC_FEATURE
<222> (423)
<223> Xaa equals any of the naturally occurring L-amino acids

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<400> 5
Met Val Thr Cys Thr Cys Leu Pro Asp Tyr Glu Gly Asp Gly Trp Ser
 1 5 10 15

Cys Arg Ala Arg Asn Pro Cys Thr Asp Gly His Arg Gly Gly Cys Ser
 20 25 30

Glu His Ala Asn Cys Leu Ser Thr Gly Leu Asn Thr Arg Arg Cys Glu
 35 40 45

Cys His Ala Gly Tyr Val Gly Asp Gly Leu Gln Cys Leu Glu Glu Ser
 50 55 60

Glu Pro Pro Val Asp Arg Cys Leu Gly Gln Pro Pro Pro Cys His Ser
 65 70 75 80

Asp Ala Met Cys Thr Asp Leu His Phe Gln Glu Lys Arg Ala Gly Val

```

85										90					95				
Phe	His	Leu	Gln	Ala	Thr	Ser	Gly	Pro	Tyr	Gly	Leu	Asn	Phe	Ser	Glu				
			100					105					110						
Ala	Glu	Ala	Ala	Cys	Glu	Ala	Gln	Gly	Ala	Val	Leu	Ala	Ser	Phe	Pro				
		115					120					125							
Gln	Leu	Ser	Ala	Ala	Gln	Gln	Leu	Gly	Phe	His	Leu	Cys	Leu	Met	Gly				
	130					135					140								
Trp	Leu	Ala	Asn	Gly	Ser	Thr	Ala	His	Pro	Val	Val	Phe	Pro	Val	Ala				
145					150					155					160				
Asp	Cys	Gly	Asn	Gly	Arg	Val	Gly	Ile	Val	Ser	Leu	Gly	Ala	Arg	Lys				
			165						170					175					
Asn	Leu	Ser	Glu	Arg	Trp	Asp	Ala	Tyr	Cys	Phe	Arg	Val	Gln	Asp	Val				
			180					185					190						
Ala	Cys	Arg	Cys	Arg	Asn	Gly	Phe	Val	Gly	Asp	Gly	Ile	Ser	Thr	Cys				
		195					200					205							
Asn	Gly	Lys	Leu	Leu	Asp	Val	Leu	Ala	Ala	Thr	Ala	Asn	Phe	Ser	Thr				
	210					215					220								
Phe	Tyr	Gly	Met	Leu	Leu	Gly	Tyr	Ala	Asn	Ala	Thr	Gln	Arg	Gly	Leu				
225					230				235						240				
Asp	Phe	Leu	Asp	Phe	Leu	Asp	Asp	Glu	Leu	Thr	Tyr	Lys	Thr	Leu	Phe				
				245				250						255					
Val	Pro	Val	Asn	Glu	Gly	Phe	Val	Asp	Asn	Met	Thr	Leu	Ser	Gly	Pro				
			260					265					270						
Asn	Leu	Glu	Leu	His	Ala	Ser	Asn	Ala	Thr	Leu	Leu	Ser	Ala	Asn	Ala				
		275					280					285							
Ser	Gln	Gly	Lys	Leu	Leu	Pro	Ala	His	Ser	Gly	Leu	Ser	Leu	Ile	Ile				
	290					295					300								
Ser	Asp	Ala	Gly	Pro	Asp	Asn	Ser	Ser	Trp	Ala	Pro	Val	Ala	Pro	Gly				
305					310					315					320				
Thr	Val	Val	Val	Ser	Arg	Ile	Ile	Val	Trp	Asp	Ile	Met	Ala	Phe	Asn				
				325					330				335						
Gly	Ile	Ile	His	Ala	Leu	Ala	Ser	Pro	Leu	Leu	Ala	Pro	Pro	Gln	Pro				
			340					345					350						
Gln	Ala	Val	Leu	Ala	Xaa	Glu	Ala	Pro	Pro	Val	Ala	Ala	Gly	Val	Gly				
		355				360						365							
Ala	Val	Leu	Ala	Ala	Gly	Ala	Leu	Leu	Gly	Leu	Val	Ala	Gly	Ala	Leu				
		370				375					380								
Tyr	Leu	Arg	Ala	Arg	Gly	Lys	Pro	Met	Gly	Phe	Gly	Phe	Ser	Ala	Phe				
385					390					395					400				
Gln	Ala	Glu	Asp	Asp	Ala	Asp	Asp	Xaa	Phe	Ser	Pro	Trp	Gln	Glu	Gly				
				405				410						415					
Thr	Asn	Pro	Xaa	Leu	Xaa	Xaa	Val	Pro	Asn	Pro	Val	Phe	Gly	Ser	Asp				
			420					425					430						

Thr Phe Cys Glu Pro Phe Asp Asp Ser Leu Leu Glu Glu Asp Phe Pro
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Asp Thr Gln Arg Ile Leu Thr Val Lys
 450 455

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 <212> PRT
 <213> Homo sapiens

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 Met Tyr Trp Asp Thr Gly Trp Gly Lys Asp Gly His Asn Ser Trp Arg
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 Ala Ala Gly Val Tyr His Arg Ala Arg Ser Gly Lys Tyr Lys Thr Tyr
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 Ala Ala Lys Ala Val Cys Gly Gly His Ala Thr Tyr Lys Ala Ala Arg
 35 40 45
 Lys Gly His Val Cys Ala Ala Gly Trp Met Ala Lys Gly Arg Val Gly
 50 55 60
 Tyr Val Lys Gly Asn Cys Gly Gly Lys Thr Gly Asp Tyr Gly Arg Asn
 65 70 75 80
 Arg Ser Arg Trp Asp Ala Tyr Cys Tyr Asn His Ala Lys Cys Gly Gly
 85 90 95
 Val Thr Asp Lys Arg Lys Ser Gly Asn Tyr Asp Asn Cys Tyr Trp His
 100 105 110
 Arg Lys Tyr Gly Arg His Ser Asp Asp Asp Asp Gly Cys Ala Asp Tyr
 115 120 125
 Val Tyr Asp Ser Tyr Asp Asp Val His Gly Val Gly Arg Tyr Cys Gly
 130 135 140
 Asp Asp Asp Ser Thr Gly Asn Val Met Thr Lys Ser Asp Ala Ser Val
 145 150 155 160
 Thr Ala Gly Gly Lys Tyr Val Ala Met Asp Val Ser Lys Ser Ser Gly
 165 170 175
 Lys Asn Thr Ser Thr Thr Ser Thr Gly Asn Lys Asn Ala Gly Arg Ser
 180 185 190

His

<210> 7
 <211> 985
 <212> DNA
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 <222> (118)..(984)

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cctgggggacg tttgccctgg ggccccagcc tggccccgggt caccctggca tgaggag 117

atg ggc ctg ttg ctc ctg gtc cca ttg ctc ctg ctg ccc ggc tcc tac 165
Met Gly Leu Leu Leu Val Pro Leu Leu Leu Leu Pro Gly Ser Tyr
1 5 10 15

gga ctg ccc ttc tac tac ggc ttc tac tac tcc aac agc gcc aac gac 213
Gly Leu Pro Phe Tyr Tyr Gly Phe Tyr Tyr Ser Asn Ser Ala Asn Asp
20 25 30

cag aac cta ggc aac ggt cat ggc aaa gac cta cnt aat gga gtg aag 261
Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Xaa Asn Gly Val Lys
35 40 45

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ctg gtg gtg gag aca ccc gag gag acc ctg ttc acc tac caa ggg gcc	309
Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala	
50 55 60	
agt gtg atc ctg ccc tgc cgc tac cgc tac gag ccg gcc ctg gtc tcc	357
Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser	
65 70 75 80	
ccg cgg cgt gtg cgt gtc aaa tgg tgg aag ctg tcg gag aac ggg gcc	405
Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala	
85 90 95	
cca gag aag gac gtg ctg gtg gcc atc ggg ctg agg cac cgc tcc ttt	453
Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe	
100 105 110	
ggg gac tac caa ggc cgc gtg cac ctg cgg cag gac aaa gag cat gac	501
Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp	
115 120 125	
gtc tcg ntg gag atc cag gnt ctg cgg ctg gag gac tat ggg cgt tac	549
Val Ser Xaa Glu Ile Gln Xaa Leu Arg Leu Glu Asp Tyr Gly Arg Tyr	
130 135 140	
cgc tgt gag gtc atn gac ggg ctg gag gat gaa agc ggt ctg gtg gag	597
Arg Cys Glu Val Xaa Asp Gly Leu Glu Asp Glu Ser Gly Leu Val Glu	
145 150 155 160	
ctg gag ctg cgg ggt gtg gtc ttt cct tac cag tcc ccc aac ggg cgc	645
Leu Glu Leu Arg Gly Val Val Phe Pro Tyr Gln Ser Pro Asn Gly Arg	
165 170 175	
tac cag ttc aac ttc cac gag ggc cag cag gtc tgt gca gag cag gct	693
Tyr Gln Phe Asn Phe His Glu Gly Gln Gln Val Cys Ala Glu Gln Ala	
180 185 190	
gcg gtg gtg gcc tcc ttt gag cag ctc ttc cgg gcc tgg gag gag ggc	741
Ala Val Val Ala Ser Phe Glu Gln Leu Phe Arg Ala Trp Glu Glu Gly	
195 200 205	
ctg gac tgg tgc aac gcg ggc tgg ctg cag gat gcc acg gtg cag tac	789
Leu Asp Trp Cys Asn Ala Gly Trp Leu Gln Asp Ala Thr Val Gln Tyr	
210 215 220	
ccc atc atg ttg ccc cgg cag ccc tgc ggt ggc ccg gac ctg gca cct	837
Pro Ile Met Leu Pro Arg Gln Pro Cys Gly Gly Pro Asp Leu Ala Pro	
225 230 235 240	
ggc gtg cga agc tac ggc ccc cgc cac cgc cgc ctg cac cgc tat gat	885
Gly Val Arg Ser Tyr Gly Pro Arg His Arg Arg Leu His Arg Tyr Asp	
245 250 255	
gta ttc tgc ttc gct act gcc ctc arg ggg cgg gtg tac tac ctg gan	933
Val Phe Cys Phe Ala Thr Ala Leu Xaa Gly Arg Val Tyr Tyr Leu Xaa	
260 265 270	
cac cct gag aan ctg acn ctg aca naa gca agg gaa gcc tgc caa gaa	981
His Pro Glu Xaa Leu Xaa Leu Thr Xaa Ala Arg Glu Ala Cys Gln Glu	
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Lys	

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<210> 8
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<213> Homo sapiens

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Gly Leu Pro Phe Tyr Tyr Gly Phe Tyr Tyr Ser Asn Ser Ala Asn Asp
      20              25              30

Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Xaa Asn Gly Val Lys
  35              40              45

Leu Val Val Glu Thr Pro Glu Thr Leu Phe Thr Tyr Gln Gly Ala
  50              55              60

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Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser
 65 70 75 80
 Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala
 85 90 95
 Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe
 100 105 110
 Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp
 115 120 125
 Val Ser Xaa Glu Ile Gln Xaa Leu Arg Leu Glu Asp Tyr Gly Arg Tyr
 130 135 140
 Arg Cys Glu Val Xaa Asp Gly Leu Glu Asp Glu Ser Gly Leu Val Glu
 145 150 155 160
 Leu Glu Leu Arg Gly Val Val Phe Pro Tyr Gln Ser Pro Asn Gly Arg
 165 170 175
 Tyr Gln Phe Asn Phe His Glu Gly Gln Gln Val Cys Ala Glu Gln Ala
 180 185 190
 Ala Val Val Ala Ser Phe Glu Gln Leu Phe Arg Ala Trp Glu Glu Gly
 195 200 205
 Leu Asp Trp Cys Asn Ala Gly Trp Leu Gln Asp Ala Thr Val Gln Tyr
 210 215 220
 Pro Ile Met Leu Pro Arg Gln Pro Cys Gly Gly Pro Asp Leu Ala Pro
 225 230 235 240
 Gly Val Arg Ser Tyr Gly Pro Arg His Arg Arg Leu His Arg Tyr Asp
 245 250 255
 Val Phe Cys Phe Ala Thr Ala Leu Xaa Gly Arg Val Tyr Tyr Leu Xaa
 260 265 270
 His Pro Glu Xaa Leu Xaa Leu Thr Xaa Ala Arg Glu Ala Cys Gln Glu
 275 280 285

Lys

<210> 9

<211> 355

<212> PRT

<213> Homo sapiens

<400> 9

Met Thr Ser Leu Leu Phe Leu Val Leu Ile Ser Val Cys Trp Ala Glu
 1 5 10 15
 Pro His Pro Asp Asn Ser Ser Leu Glu His Glu Arg Ile Ile His Ile
 20 25 30
 Gln Glu Glu Asn Gly Pro Arg Leu Val Val Ala Glu Gln Ala Lys
 35 40 45
 Ile Phe Ser Gln Arg Gly Gly Asn Val Thr Leu Pro Cys Lys Phe Tyr
 50 55 60
 His Glu His Thr Ser Thr Ala Gly Ser Gly Thr His Lys Ile Arg Val

65	70					75					80				
Lys	Trp	Thr	Lys	Leu	Thr	Ser	Asp	Tyr	Leu	Lys	Glu	Val	Asp	Val	Phe
				85					90					95	
Val	Ala	Met	Gly	His	His	Arg	Lys	Ser	Tyr	Gly	Lys	Tyr	Gln	Gly	Arg
			100					105					110		
Val	Phe	Leu	Arg	Glu	Ser	Ser	Glu	Asn	Asp	Ala	Ser	Leu	Ile	Ile	Thr
		115					120					125			
Asn	Ile	Met	Leu	Glu	Asp	Tyr	Gly	Arg	Tyr	Lys	Cys	Glu	Val	Ile	Glu
	130					135					140				
Gly	Leu	Glu	Asp	Asp	Thr	Ala	Val	Val	Ala	Leu	Asn	Leu	Glu	Gly	Val
	145				150					155					160
Val	Phe	Pro	Tyr	Ser	Pro	Arg	Leu	Gly	Arg	Tyr	Asn	Leu	Asn	Phe	His
				165					170					175	
Glu	Ala	Gln	Gln	Ala	Cys	Leu	Asp	Gln	Asp	Ser	Ile	Ile	Ala	Ser	Phe
			180					185					190		
Asp	Gln	Leu	Tyr	Glu	Ala	Trp	Arg	Ser	Gly	Leu	Asp	Trp	Cys	Asn	Ala
		195					200					205			
Gly	Trp	Leu	Ser	Asp	Gly	Ser	Val	Gln	Tyr	Pro	Ile	Thr	Lys	Pro	Arg
	210					215					220				
Glu	Pro	Cys	Gly	Gly	Lys	Asn	Thr	Val	Pro	Gly	Val	Arg	Asn	Tyr	Gly
	225				230					235					240
Phe	Trp	Asp	Lys	Glu	Arg	Ser	Arg	Tyr	Asp	Val	Phe	Cys	Phe	Thr	Ser
				245					250					255	
Asn	Phe	Asn	Gly	Arg	Phe	Tyr	Tyr	Leu	Ile	His	Pro	Thr	Lys	Leu	Thr
			260					265					270		
Tyr	Asp	Glu	Ala	Val	Gln	Ala	Cys	Leu	Lys	Asp	Gly	Ala	Gln	Ile	Ala
		275					280					285			
Lys	Val	Gly	Gln	Ile	Phe	Ala	Ala	Trp	Lys	Leu	Leu	Gly	Tyr	Asp	Arg
	290					295				300					
Cys	Asp	Ala	Gly	Trp	Leu	Ala	Asp	Gly	Ser	Val	Arg	Tyr	Pro	Ile	Ser
	305				310					315					320
Arg	Pro	Arg	Lys	Arg	Cys	Ser	Pro	Asn	Glu	Ala	Ala	Val	Arg	Phe	Val
				325					330					335	
Gly	Phe	Pro	Asp	Lys	Lys	His	Lys	Leu	Tyr	Gly	Val	Tyr	Cys	Phe	Arg
			340					345					350		
Ala	Tyr	Asn													
		355													

<210> 10
 <211> 1259
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<220>
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 <222> (199)..(1257)

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gccagatgct ccagaaggc cacgaaggtc tcctgcagct gccagaaggg atacaaaggg 120
gacgggcaca gctgcacaga gatagacccc tgtgcagacg gccttaacgg aggggtgtcac 180
gagcacgcca cctgtaag atg aca ggc ccg ggc aag cac aag tgt gag tgt 231
          Met Thr Gly Pro Gly Lys His Lys Cys Glu Cys

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	1	5	10	
aaa agt cac tat gtc gga gat ggg ctg aac tgt gag ccg gag cag ctg				279
Lys Ser His Tyr Val Gly Asp Gly Leu Asn Cys Glu Pro Glu Gln Leu	15	20	25	
ccc att gac cgc tgc tta cag gac aat ggg cag tgc cat gca gac gcc				327
Pro Ile Asp Arg Cys Leu Gln Asp Asn Gly Gln Cys His Ala Asp Ala	30	35	40	
aaa tgt gtc gac ctc cac ttc cag gat acc act gtt ggg gtg ttc cat				375
Lys Cys Val Asp Leu His Phe Gln Asp Thr Thr Val Gly Val Phe His	45	50	55	
cta cgc tcc cca ctg ggc cag tat aag ctg acc ttt gac aaa gcc aga				423
Leu Arg Ser Pro Leu Gly Gln Tyr Lys Leu Thr Phe Asp Lys Ala Arg	60	65	70	75
gag gcc tgt gcc aac gaa gct gcg acc atg gca acc tac aac cag ctc				471
Glu Ala Cys Ala Asn Glu Ala Ala Thr Met Ala Thr Tyr Asn Gln Leu	80	85	90	
tcc tat nnc cag aag gcc aag tac cac ctg tgc tca gca ggc tgg ctg				519
Ser Tyr Xaa Gln Lys Ala Lys Tyr His Leu Cys Ser Ala Gly Trp Leu	95	100	105	
gag acc ggg cgg gtt gcc tac ccc aca gcc ttc gcc tcc cag aac tgt				567
Glu Thr Gly Arg Val Ala Tyr Pro Thr Ala Phe Ala Ser Gln Asn Cys	110	115	120	
ggc tct ggt gtg gtt ggg ata gtg gac tat gga cct aga ccc aac aag				615
Gly Ser Gly Val Val Gly Ile Val Asp Tyr Gly Pro Arg Pro Asn Lys	125	130	135	
agt gaa atg tgg gat gtc ttc tgc tat cgg atg aaa gat gtg aac tgc				663
Ser Glu Met Trp Asp Val Phe Cys Tyr Arg Met Lys Asp Val Asn Cys	140	145	150	155
acc tnc aag gtg ggc tat gtg gga gat ggc ttc tca tac agt ggg aac				711
Thr Xaa Lys Val Gly Tyr Val Gly Asp Gly Phe Ser Tyr Ser Gly Asn	160	165	170	
ctg ctg cag gtc ctg atg tcc ttc ccc tca ctc aca aac ttc ctg acg				759
Leu Leu Gln Val Leu Met Ser Phe Pro Ser Leu Thr Asn Phe Leu Thr	175	180	185	
gaa gtg ctg gcc tat tcc aac agc tca gct cga ggc cgt gca ttt cta				807
Glu Val Leu Ala Tyr Ser Asn Ser Ser Ala Arg Gly Arg Ala Phe Leu	190	195	200	
gaa cac ctg act gac ctg tcc atc cgc ggc acc ctc ttt gtn cca cag				855
Glu His Leu Thr Asp Leu Ser Ile Arg Gly Thr Leu Phe Val Pro Gln	205	210	215	
aac agt ggg ctg ggg gag aat gag acc ttg tct ggg cgg gac atc gag				903
Asn Ser Gly Leu Gly Glu Asn Glu Thr Leu Ser Gly Arg Asp Ile Glu	220	225	230	235
cac cac ctc gcc aat gtc agc atg ttt ttc tac aat gac ctt gtc aat				951
His His Leu Ala Asn Val Ser Met Phe Phe Tyr Asn Asp Leu Val Asn	240	245	250	
ggc acc acc ctg caa acg agg ctg gga agc aag ctg ctc atc act gac				999
Gly Thr Thr Leu Gln Thr Arg Leu Gly Ser Lys Leu Leu Ile Thr Asp				

	255		260		265	
aga cag gac cca ctc cac ccg acg gag acc agg tgt gtt gat gga aga						1047
Arg Gln Asp Pro Leu His Pro Thr Glu Thr Arg Cys Val Asp Gly Arg						
	270		275		280	
gac act ctg gag tgg gac atc tgt gcc tcc aat ggg atc aca cat gtc						1095
Asp Thr Leu Glu Trp Asp Ile Cys Ala Ser Asn Gly Ile Thr His Val						
	285		290		295	
att tcc agg yct tta aaa gca ccc cct gcc ccc gtg acc ttg ncc cac						1143
Ile Ser Arg Xaa Leu Lys Ala Pro Pro Ala Pro Val Thr Leu Xaa His						
	300		305		310	315
act ggn ttg gga gna ggg atc ttc tnt gnc atc atc ctg gtg act ggg						1191
Thr Gly Leu Gly Xaa Gly Ile Phe Xaa Xaa Ile Ile Leu Val Thr Gly						
		320		325		330
gct gtt gcc ttg gct gct tac tcc tac ttt cgg ata aac cgg aaa aca						1239
Ala Val Ala Leu Ala Ala Tyr Ser Tyr Phe Arg Ile Asn Arg Lys Thr						
		335		340		345
atc ggc ttc can cat ttt ga						1259
Ile Gly Phe Xaa His Phe						
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<210> 11
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 <212> PRT
 <213> Homo sapiens

<220>
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          20          25          30

Leu Gln Asp Asn Gly Gln Cys His Ala Asp Ala Lys Cys Val Asp Leu
          35          40          45

His Phe Gln Asp Thr Thr Val Gly Val Phe His Leu Arg Ser Pro Leu
          50          55          60

Gly Gln Tyr Lys Leu Thr Phe Asp Lys Ala Arg Glu Ala Cys Ala Asn
 65          70          75          80

Glu Ala Ala Thr Met Ala Thr Tyr Asn Gln Leu Ser Tyr Xaa Gln Lys
          85          90          95

Ala Lys Tyr His Leu Cys Ser Ala Gly Trp Leu Glu Thr Gly Arg Val
          100          105          110

Ala Tyr Pro Thr Ala Phe Ala Ser Gln Asn Cys Gly Ser Gly Val Val
          115          120          125

Gly Ile Val Asp Tyr Gly Pro Arg Pro Asn Lys Ser Glu Met Trp Asp
          130          135          140

Val Phe Cys Tyr Arg Met Lys Asp Val Asn Cys Thr Xaa Lys Val Gly
          145          150          155          160

Tyr Val Gly Asp Gly Phe Ser Tyr Ser Gly Asn Leu Leu Gln Val Leu
          165          170          175

Met Ser Phe Pro Ser Leu Thr Asn Phe Leu Thr Glu Val Leu Ala Tyr
          180          185          190

Ser Asn Ser Ser Ala Arg Gly Arg Ala Phe Leu Glu His Leu Thr Asp
          195          200          205

Leu Ser Ile Arg Gly Thr Leu Phe Val Pro Gln Asn Ser Gly Leu Gly
          210          215          220

Glu Asn Glu Thr Leu Ser Gly Arg Asp Ile Glu His His Leu Ala Asn
          225          230          235          240

Val Ser Met Phe Phe Tyr Asn Asp Leu Val Asn Gly Thr Thr Leu Gln
          245          250          255

Thr Arg Leu Gly Ser Lys Leu Leu Ile Thr Asp Arg Gln Asp Pro Leu
          260          265          270

His Pro Thr Glu Thr Arg Cys Val Asp Gly Arg Asp Thr Leu Glu Trp
          275          280          285

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Asp Ile Cys Ala Ser Asn Gly Ile Thr His Val Ile Ser Arg Xaa Leu
 290 295 300
 Lys Ala Pro Pro Ala Pro Val Thr Leu Xaa His Thr Gly Leu Gly Xaa
 305 310 315 320
 Gly Ile Phe Xaa Xaa Ile Ile Leu Val Thr Gly Ala Val Ala Leu Ala
 325 330 335
 Ala Tyr Ser Tyr Phe Arg Ile Asn Arg Lys Thr Ile Gly Phe Xaa His
 340 345 350

Phe

<210> 12
 <211> 275
 <212> PRT
 <213> Mus musculus

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 Gly Trp Gly Phe Lys Asn Gly Ile Phe His Asn Ser Ile Trp Leu Glu
 20 25 30
 Gln Ala Ala Gly Val Tyr His Arg Glu Ala Arg Ala Gly Arg Tyr Lys
 35 40 45
 Leu Thr Tyr Ala Glu Ala Lys Ala Val Cys Glu Phe Glu Gly Gly Arg
 50 55 60
 Leu Ala Thr Tyr Lys Gln Leu Glu Ala Ala Arg Lys Ile Gly Phe His
 65 70 75 80
 Val Cys Ala Ala Gly Trp Met Ala Lys Gly Arg Val Gly Tyr Pro Ile
 85 90 95
 Val Lys Pro Gly Pro Asn Cys Gly Phe Gly Lys Thr Gly Ile Ile Asp
 100 105 110
 Tyr Gly Ile Arg Leu Asn Arg Ser Glu Arg Trp Asp Ala Tyr Cys Tyr
 115 120 125
 Asn Pro His Ala Lys Glu Cys Gly Gly Val Phe Thr Asp Pro Lys Arg
 130 135 140
 Ile Phe Lys Ser Pro Gly Phe Pro Asn Glu Tyr Asp Asp Asn Gln Val
 145 150 155 160
 Cys Tyr Trp His Ile Arg Leu Lys Tyr Gly Gln Arg Ile His Leu Ser
 165 170 175
 Phe Leu Asp Phe Asp Leu Glu His Asp Pro Gly Cys Leu Ala Asp Tyr
 180 185 190
 Val Glu Ile Tyr Asp Ser Tyr Asp Asp Val His Gly Phe Val Gly Arg
 195 200 205
 Tyr Cys Gly Asp Glu Leu Pro Glu Asp Ile Ile Ser Thr Gly Asn Val
 210 215 220
 Met Thr Leu Lys Phe Leu Ser Asp Ala Ser Val Thr Ala Gly Gly Phe
 225 230 235 240

Gln Ile Lys Tyr Val Thr Val Asp Pro Ala Ser Lys Ser Ser Gln Ala
245 250 255
Lys Asn Thr Ser Thr Thr Gly Asn Lys Lys Phe Leu Pro Gly Arg Phe
260 265 270
Ser His Leu
275

<210> 13
<211> 44
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<220>
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<400> 13
gcagcaggat ccatgatgga ccagggctgc cgggaaatcc ttac 44

<210> 14
<211> 44
<212> DNA
<213> artificial sequence

<220>
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<400> 14
gcagcatcta gatcacttga ctgtgaggat cctctgggtg tcag 44

<210> 15
<211> 45
<212> DNA
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<220>
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<210> 16
<211> 45
<212> DNA
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<220>
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<210> 17
<211> 48
<212> DNA
<213> artificial sequence

<220>
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 <210> 18
 <211> 46
 <212> DNA
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 <220>
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 <222> (40)
 <223> n equals a, t, g or c
 <220>
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 <400> 18
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 <210> 19
 <211> 44
 <212> DNA
 <213> artificial sequence
 <220>
 <223> contains an EcoRI restriction site
 <400> 19
 gcagcaggat ccatgacagg cccgggcaag cacaagtgtg agtg 44
 <210> 20
 <211> 49
 <212> DNA
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 <220>
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 <222> (21)
 <223> n equals a, t, g or c
 <220>
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 <400> 20
 gcagcatcta gatcaaaatg ntggaagccg attgttttcc ggtttatcc 49
 <210> 21
 <211> 50
 <212> DNA
 <213> artificial sequence
 <220>
 <223> contains a BglII restriction site
 <400> 21
 gcagcaagat ctgccatcat gatggaccag ggctgccggg aaatccttac 50

<210> 22
 <211> 45
 <212> DNA
 <213> artificial sequence

 <220>
 <223> contains a XbaI restriction site

 <400> 22
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 <210> 23
 <211> 51
 <212> DNA
 <213> artificial sequence

 <220>
 <223> contains a BglII restriction site

 <400> 23
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 <210> 24
 <211> 45
 <212> DNA
 <213> artificial sequence

 <220>
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 <400> 24
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 <210> 25
 <211> 54
 <212> DNA
 <213> artificial sequence

 <220>
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 <400> 25
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 <212> DNA
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 <220>
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 <220>
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 <400> 26
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<210> 27
 <211> 50
 <212> DNA
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 <223> contains a BglIII restriction site

 <400> 27
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 <210> 28
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 <400> 28
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 <210> 29
 <211> 50
 <212> DNA
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 <223> contains a BamHI restriction site

 <400> 29
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 <210> 30
 <211> 44
 <212> DNA
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 <223> contains an XbaI restriction site

 <400> 30
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 <210> 31
 <211> 54
 <212> DNA
 <213> artificial sequence

 <220>
 <223> contains a BamHI restriction site

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<210> 32
 <211> 45
 <212> DNA
 <213> artificial sequence

 <220>
 <223> contains an XbaI restriction site

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 <210> 33
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 <220>
 <223> contains a BamHI restriction site

 <400> 33
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 <220>
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 <210> 35
 <211> 50
 <212> DNA
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 <220>
 <223> contains a BamHI restriction site

 <400> 35
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 <210> 36
 <211> 49
 <212> DNA
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 <220>
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 <223> n equals a, t, g or c

<220>

<223> contains an XbaI restriction site

<400> 36

gcagcatcta gatcaaatg ntggaagccg attgttttcc ggtttatcc

49

<210> 37

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<212> DNA

<213> Homo sapiens

<400> 37

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tcaagttcaa	ctggtacgtg	gacggcgtgg	aggtgcataa	tgccaagaca	aagccgcggg	240
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ggctgaatgg	caaggagtac	aagtgcaagg	tctccaacaa	agccctocca	accccatcg	360
agaaaaccat	ctccaaagcc	aaagggcagc	cccagagaacc	acaggtgtac	accctgcccc	420
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